

A variety of interactions in the marine environment

ABSTRACTS VOLUME FROM 49TH EUROPEAN MARINE BIOLOGY SYMPOSIUM

September 8–12, 2014 St. Petersburg, Russia

Zoological Institute Russian Academy of Sciences

The ratio of body parts (shell, soft tissues, mantle fluid) and tissue biochemical composition in mussels largely depends on their reproductive cycle, which is associated mainly with seasonal course of water temperature. Mussels from the Sea of Okhotsk and the Pechora Seas had higher content of soft tissues (25-30 %) compared to the White Sea mollusks (15-20%). Proteins made up 50-60% of dry weight tissue in White Sea mussels and 70 % for those from the Sea of Okhotsk. Glycogen content in the White Sea mussels was significantly higher than that of mussels from the Pechora Sea and Sea of Okhotsk. Maximum values were observed in summer in post-spawning period when available food concentration was maximal followed by a slow spending of glycogen reserves in autumn and winter. Seasonal variation in lipid content was opposite to glycogen levels in tissues. On average, mussel dry tissues contained about 8-12% of lipids. In the period of active gonad maturation and preparation for spawning glycogen concentrations decreased rapidly accompanied by a sharp increase in the proportion of lipids, indicating the conversion of glycogen to lipids in oocyte maturation.

We determined the average number and size of mussels in the crops of king eiders *Somateria spectabilis* and common eiders *S. mollissima* and calculated the total energy content of mussels consumed at once by actively feeding birds. Taking into account the caloric value of mussels in the studied areas it appeared that the birds feeding in the White Sea should consume about 40% more mussels than in the Sea of Okhotsk for getting the same amount of energy. We assume that differences in nutritional value and energy content of mussels from different waters may account for the degree of impact of migratory birds on mussels coastal populations.

This work was supported by grants INTAS # 05-1000008-8056, RFBR 14-04-00466 and 14-04-10022-k.

ATTACHMENT STRATEGY OF *ELEUTHEROSCHIZON DUBOSCQI* (APICOM-PLEXA): A PROTOCOCCIDIAN SHARING FEATURES OF GREGARINES AND CRYPTOSPORIDIA

A. Valigurova¹, G. G. Paskerova², A. Diakin¹, T. G. Simdyanov³

¹Department of Botany and Zoology, Faculty of Science, Masaryk University, Brno, Čzech Republic ²Department of Invertebrate Zoology, Faculty of Biology, Saint-Petersburg State University, St. Petersburg, Russia ³Department of Invertebrate Zoology, Faculty of Biology, Lomonosov Moscow State University, Russia

Apicomplexa represent very successful group of unicellular parasites that evolved unique adaptations for invading and surviving within their hosts. In contrast to well-studied etiologic agents of significant human diseases (e.g. malaria, cryptosporidiosis), apicomplexans restricted to invertebrates remain poorly understood. Nevertheless, they appear to be very important in the comprehension of evolutionary pathways and phylogenetic relations within the phylum Apicomplexa. It is assumed that ancestral apicomplexans parasitized marine annelids, and their adaptation to the parasitic life style and further radiation took place before the era of vertebrates. At the beginning they spread to other marine invertebrates, then to freshwater and terrestrial invertebrates, and finally to vertebrates. Their zoite exhibits a high degree of polarity in that it has an apical pole equipped with a unique complex, comprising specialized secretory organelles, polar rings, and a conoid. This invasion apparatus traditionally used as the best defining feature for Apicomplexa, can be also found in other Myzozoa. Apicomplexan evolution most likely progressed from myzocytotic predation to myzocytotic extracellular parasitism (e.g. gregarines, cryptosporidia), and finally to intracellular parasitism typical for coccidia. The origination of extracellular parasitism in gregarines resulted in improvement of their attachment apparatus, which exhibits an enormous diversity in architecture. Recent studies pointed out the unique epicellular localization of cryptosporidia within extraordinary host cell-derived parasitophorous sac, and the similarity in their attachment and feeding strategy with gregarines; i.e. both groups form a specialized host-parasite interface and reflect analogous modes of adaptation to similar environment within host. Based on phylogenetic analyses reporting close affinity of gregarines and cryptosporidia, speculation that cryptosporidia represent a 'missing link' between the gregarines and coccidia is frequently discussed. This study focuses on attachment strategy, cell cortex and cytoskeleton of protococcidian Eleutheroschizon duboscqi Brasil, 1906, a representative of marine deep-branching apicomplexans, which shares features of both the gregarines and coccidia. Littoral samples of host polychaete Scoloplos (Scoloplos) armiger Müller, 1776 were collected at the Nikolai Pertsov White Sea Biological Station of MSU (Velikaya Salma straight, Kandalaksha Gulf, White Sea). The helmet-shaped stages attached to the host cell show more or less distinct metabolic activity. Attached parasites are covered by a parasitophorous sac (PS) resembling that of cryptosporidia. The caudal part of the PS forms a short tipped appendage, a tail. The attachment apparatus consists of several short projections (lobes) arranged in circles, surrounded by another circle of filamentous fascicles. No organelles of apical complex were observed. Cell surface exhibits shallow grooves with micropores at their bottom. The parasite pellicle seems to be trilaminar, but the membranes are difficult to discern. The phalloidin labelling for confocal laser scanning microscopy (CLSM) confirmed the high accumulation of filamentous actin (Factin) in a brush border of host epithelium and in two layers at the parasite periphery; the outer one seems to correspond to the PS that is considered of host cell origin (including the attachment site) and the inner less distinct layer that could correspond to the layer of short filaments underling the parasite pellicle observed under electron microscopy. The tail formed from the caudal part of the PS exhibited signal of medium intensity for F-actin. The cytoplasm of parasites exhibited F-actin signal of lower intensity, similarly to cytoplasm of epithelial cells. The staining with Evans Blue viewed under CLSM revealed a relatively high concentration of unspecified proteins in the PS tail and in the area of attachment site. During experiments with membrane-permeable probes influencing the polymerization of cytoskeletal proteins, G-actin into actin filaments (jasplakinolide, cytochalasin D) and α -tubulin in microtubules (oryzalin), parasites not only survived incubation in very high doses of these drugs and but also showed signs of motility within their sacs for next couple of hours. After treatment with jasplakinolide (stabilizes actin filaments, induces actin polymerisation) the F-actin staining became brighter in the area of the PS, while specimens treated for long period in cytochalasin D (disrupts actin filaments, inhibits actin polymerisation) exhibited almost no F-actin labelling. Parasites labelled with the specific anti-actin antibody (known to recognize Toxoplasma actin) exhibited only indistinct fluorescence signal. The immunolocalization of actin differed from phalloidin labelling in that the antibody did not label the PS, but labelled the host tissue with the same intensity as parasite inside the PS. A weak staining of the PS tail was observed in all individuals. The myosin labelling was restricted to the periphery of the PS. The immunolabelling with an anti-a-tubulin antibody used for visualization of subpellicular microtubules and related structures was strongly positive for brush border of host intestinal epithelium. Despite the fact that under electron microscopy no typical microtubules were observed, both the surface of the parasite itself and the PS exhibited relatively distinct labelling. After prolonged incubation of living parasites in oryzalin (disrupts microtubules), the peripheral labelling gradually decreased through more diffuse to very weak as if putatively unpolymerised form of α-tubulin dispersed throughout the cytoplasm. Detailed electron microscopic analysis revealed that E. duboscqi attachment strategy shares features of cryptosporidia and gregarines, i.e. it conspicuously resembles an epicellularly located gregarine embraced by PS, which seems to develop in similar manner as shown in cryptosporidia. Interestingly, the membranes of parasite pellicle become disorganized during its early development, and the interface between PS and parasite remains unclear. In advanced developmental stages, the space between PS and parasite pellicle appears translucent with tiny filamentous structures and it resembles the cortical vesicle of gregarine epimerite, even though it envelopes the entire parasite up to the PS tail. We also speculate that attached individuals preserve their PS until the end of development, even if they eventually detach from host tissue.

We acknowledge the financial support from ECIP - Centre of excellence, GAČR No. GBP505/12/G112.

ATLANTIC HERRING FRESH FROM THE CELTIC SEA – THE CHEF'S SUGGESTION ON TODAY'S WHALE MENU M. Volkenandt¹, S. Berrow², I. O'Connor², J.-M. Guarini¹ ¹Universite Pierre et Marie Curie, UMR 8222 - LECOB, Banyuls sur mer, France ²Galway-Mayo Institute of Technology, MFRC, Galway, Ireland

Atlantic herring (*Clupea harengus*) is an important pelagic key species within the Celtic Sea ecosystem. It is favourite prey for sea birds and cetaceans, and of high value for the Irish fishery industries. Over the last years, the Celtic Sea herring stock has been increasing, and simultaneously increased the number of land-based sightings for fin and humpback whales (Balaenoptera physalus and Megaptera novaeangliae). It is difficult to differentiate between an increase in abundance, or a higher rate of resigntings of the same whales. Both whale species have been observed lunge feeding in herring spawning grounds and dietary studies indicate a high importance of herring within their diet. Here, we simulate trajectories of whales in the Celtic Sea during herring spawning migration. A dynamic model was developed to investigate the co-occurrence of predator and prey and the model output was compared to eight years of visual observations in the field. First, the distribution of energy provided by herring was analysed and quantified as a forcing factor. Then, the movement of predators, including behaviour changes, i.e. diving and feeding, has been simulated, using an oriented random walk process. The model represents a theoretical distribution of a top predator and its prey and includes predation interactions. Predation is governed by processed derived from dynamic energy budgets in a framework of optimal foraging, although the loss of energy during foraging was seen as a deterministic feature and energy gain remained a stochastic component important to include in the simulation process. Results of the simulations provide valuable information